

Supplementary Data

Peptide sequences identified by MS MS sequencing and corresponding to carbonylated proteins in Arabidopsis seeds and during germination. The proteins identified correspond to those listed in Table I of the submitted manuscript.

N°	Protein name	AGI locus name	Peptide sequences identified	% Cov.
39	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	At3g04120	IGINGFGR YDSVHGQWK TLLFGEKPVTVF GIR KVVISAPSK AASFNIIPSSTGAAK VLPALNGK VLPALNGK Deamidation N (6) AATYDEIKK Methyl LVSWYDNEWGYSSR	25%
40	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	At3g04120	TVDGPSMKDWR + Oxidation (M) AASFNIIPSSTGAAK VPTVDVSVVDLTVR TLLFGEK PVTVFGIR LVSWYDNEWGYSSR FGIVEGLMTTVHISITATQK + Oxidation (M) DEKTLFGEK PVTVFGIR GILGYTEDDVVSTDFVG DNR	32%
84	Alpha-globulin 12S (Seed storage protein At5g44120 fragment)		GLYLPSSFNTAK VQGPFGVIRPPLR IEVWDHHAPQLR NIFNGFGPEVIAQALK IDLQTAQQQLQNQDDNR SEGGRIEVWDHHAPQLR TNANAQINTLAGRTS VL R VIPGCAETFQDSSEFQPR NPRPFYLAGNNPQGQVWLQGR	55%
92	Jasmonate inducible protein-like	At2g33070	FVLQGGK IVGFHGR GGAGLEVVQGK EIISTLTFK TSPPFGIVSGTK CSHDIAQVG NK + Carbamidomethyl (C) LGEEEETPSIR TLDAYNIVDH K HLYVFDLETR VYVGQGEDGIAFVK LKTLDAYNIVDH K	25%
98	Beta-cruciferin 12S (seed storage protein At1g03880 fragment)		FQWVEFK CTDNLDDPSR + Carbamidomethyl (C) TNANAQINTLAGR ATSNRFQWVEFK GLPLEVITNGFQISPEEAR GLPLEVITNGFQISPEEARR VFDGQVSQGQLIAVPQGFSVVKR ADVYKPQLGYISTLNSYDLPILR	45%

105 Elongation factor 1-gamma 2	At1g57720	ALIAAEYAGVK FTSAFPHVER MLICGSEGPFK + Carbamidomethyl (C); Oxidation (M) KFTSAFPHVER	10%
128 Elongation factor 1-beta-gamma	At1g09640	ALVLHTYK + Acetyl (N-term) FTSEFPHVER MLICGSEGPFK + Carbamidomethyl (C); Oxidation (M) YNDENMVSFVTLNK + Oxidation (M)	10%
129 Eukaryotic initiation factor 4A-1	At3g13920 or At1g72730	ALGDYLGVK GLDVIQQAQSGTAK MFVLDEADEMLSR + 2 Oxidation (M) KGVAINFVTRDDER GIYAYGFEKPSAIQQR 28%	16%
131 Aldose reductase	At5g01670	VRPALQNTLK DLIHDTQTVDR WGLQRGTSVIPK LLSGHKIPAVGLGTWR VIDGEDLFVNKTTEGPFR	20%
151 Cupin family protein	At1g03890	ENQLDQVPR ASYGVNEEEAKR ANGPLHFVIPPPR ISTLNSLNLPVLR GDSDAVIVIVLDVTNR GDVFASLAGVSQWWYNR TNDNAYINTLSGQTSYLR FEAGQMEVWDHMSPELR + 2 Oxidation (M) RGDVFAASLAGVSQWWYNR EAPFPNACHFSQINSLAPAQATK	34%
177 12S seed storage protein [Precursor]	At1g03880	VNGPFGVIRPPLR HAIGEQFEWIEFK INVETAQQLQNQQDNR SEGGRIEVWDHAPQLR GLPLEVITNGYQISPEEAKR INVETAQQLQNQQDNRGNIVK TNENAQVNTLAGR	25%
194 3-oxoacyl-[acyl-carrier-protein] synthase 1. chloroplast [Precursor]	At5g46290	LLSGESGISLIDR ADGLGVSSCIER + Carbamidomethyl (C) GFSSEGYIDGKNER ALESANLGGDKLNTIDKR KQHEVDVAISNSFGFGGHNSVVAFSAFKP AINTGWLHPSINQFNPEQAVDFDTVNEK	24%
210 Low-temperature-induced 65 kDa protein or Desiccation-responsive protein 29B	At5g52300	GVTAKNYISEK TFAPGGEDDYLGGQR EAPTHYPLGVSEFSDR DLPTGTHDQFSPESLRPK EAPTHYPLGVSEFSDRGESR EAHQEPPLNTPVSLLSATEDVTR RLEEDPAAPGGGSDYLSGVSNYQSK	18%
216 Glycosyl hydrolase family 1 protein	At3g21370	LSISWPR FGVYYIDFK NHNDAEAVDFYHR WLSEFLKPGLKPSK NWITFNEPWVFSR NPTWATDALVEFEPK VKNHNADEAVDFYHR VDSRNPTWATDALVEFEPK LKDSTDFVGINYTSFFAK IGIAHSPAWFEPEDVEGGQATVNR SGFEPYVVSHNLLVGHAEAVDAFR SGFEPYVVSHNLLVGHAEAVDAFRK	26%

233 Beta-cruciferin 12S (seed storage protein At5g44120 precursor fragment)	FQWVEFK GLPLEVITNGFQISPEEAR GLPLEVITNGFQISPEEARR FNTLETTLTHSSGPASYGRPR VFDGQVSQGQLIAVPQGFSVVKR VFDGQVSQGQLIAVPQGFSVVKR VKFNTLETTLTHSSGPASYGRPR	52%
238 Alpha-globulin 12S (Seed storage protein At5g44120 fragment)	GLYLPFFNTAK VQGPFGVIRPPLR IEVWDHHAPQLR IDLQTAQQQLQNQDDNRR TNANAQINTLAGRTSVLR VIPGCAETFQDSSEFQPR NPRPFYLAGNNPQGQVWLQGR IDLQTAQQQLQNQDDNRRGNIVR	28%
240 Alpha-globulin 12S (Seed storage protein At1g03880 fragment)	VNGPFGVIRPPLR IEVWDHHAPQLR VNGPFGVIRPPLR INVETAQQQLQNQQDNR SEGGRIEVWDHHAPQLR NLRPFLIAGNNPQGQEWLQGR	16%
241 Alpha-globulin 12S (Seed storage protein At4g28520 fragment)	GPFQVVRPPLR ISYVVQGTGISGR VKGPFQVVRPPLR IDVQLAQQLQNQQDNR HPRSPQGNGLEETICSMR SEAGQIEYWDHNHPQLR QGQQGQPWEQQGQQGQQGFR VFHLAGNNQGGFGGSQQQQEQK	32%
246 Storage proteins 7S	At3g22640 HAPALFR EIGQGIIR SFSDWFQSK EVLSTSFNVPEELLGR TFLAGEENLLSNLNPAATR DYFFPAASQFQQSYFNGFTK TTFVTFVENGCARFEMATPYK RPGGGSGEGWEEESTNHPYHFR RRPGGGSGEGWEEESTNHPYHFR	25%
259 Expressed protein	At1g05510 QFGVSIDKER EVDIKPVESVPR GGFLMPGVPEAIQR + Oxidation (M) ETEKQFGVSIDKER DGQLYPPEMIKETEK + Oxidation (M) QVEAHHFCGHINEDMR + Oxidation (M)	21%
290 Aconitase hydratase cytoplasmic	At4g35830 ILLESAIR IDKLPPYSIR QVEIPFKPAR ADWHSCLDNR DTIILAGAEYGSGSSR SENAVQANMELEFQR	7%
295 Peptidase M1 family protein,	At1g63770 TLLGTQGFR TLLGTQGFRK STEAYVFDHSNMAR SSGNFCTQCEAEGFR SSGNFCTQCEAEGFRK	5%

296 Pyruvate,orthophosphate dikinase	At4g15530	FAYDSFR SDFEGIFR GQEFPSPDK LWMLQCRAFK LSEVNPMMLGFR ASLDILLPYQR LGISYPELTEMQAR DIGASLADPSKPLLSVR	9%
297 Cell division cycle protein (CDC48)	At3g09840	KGDLFLVR DFSTAILER GILLYGPPGSGK KYQAFQAQTLQQSR ELVELPLRHPQLFK VRLGDVISVHQCPDVK YTQGFSGADITEICQR EIDIGVPDEIGRLEVLR DTVCIALADETCEEPKIR QSAPCVLFFDELDSIATQR	23%
319 Ribulose bisphosphate carboxylase large chain [Precursor] or rubisco	AtCg00490	QKNHGMHFR + Oxidation (M) DNGLLLHIHR DLAVEGNEIIR ALAALRLEDLR LEDLRIPPAYTK TFQGPPPHGIQVER YGRPLLGCCTIKPK GGLDFTKDDENVNSQPFMR GGLDFTKDDENVNSQPFMR + Oxidation (M) LTYYTPEYETKDTDILAAFR	26%
320 Ribulose bisphosphate carboxylase large chain [Precursor] or rubisco	AtCg00490	QKNHGMHFR + Oxidation (M) DNGLLLHIHR TFQGPPPHGIQVER YGRPLLGCCTIKPK EITFNFTIDKLDGQE GGLDFTKDDENVNSQPFMR + Oxidation (M) LTYYTPEYETKDTDILAAFR	21%
321 Ribulose bisphosphate carboxylase large chain [Precursor] or rubisco	AtCg00490	LGLSAKNYGR QKNHGMHFR + Oxidation (M) ALAALRLEDLR FLFCAEAIYK LEDLRIPPAYTK YGRPLLGCCTIKPK DRFLFCAEAIYK NEGRDLAVEGNEIIR TFQGPPPHGIQVERDK GGLDFTKDDENVNSQPFMR + Oxidation (M) LTYYTPEYETKDTDILAAFR	30%
333 Elongation factor EF-2	At1g56070	FFAFGR IMGPNYIPGEKK VIYASQITAKPR LWGENFFDPATR LWGENFFDPATRK QIIATCMNDQKDK + Oxidation (M) ILAEEFGWDKDLAK AYLPVVESFGFSSQLR NATLTNEKEVDAHPIR	20%
349 Malate oxidoreductase or Malic enzyme	At2g19900	QYQFPLQK GLLPPVVLQDK YMALTELQERNER + Oxidation (M) AIFASGSPFDPVEYEGK	8%

375 UDP-glucose pyrophosphorylase	At5g17310	SGFINLVR VLQLETAAGAAIR FFDNAIGVNPR SNVDIHTFNQSK YLSGEAQHIEWSK VVADEFVPWPSKGK FKSIPSIVELDLSK IQTPTDEIVV PYDK TNPTNPAIELGPEFK TNPTNPAIELGPEFKK LVEADALKMEIIPNPK + Oxidation (M) SNVDIHTFNQSKYPR EVDGVKVLQLETAAGAAIR VQLLEIAQVPDEHVNEFK ATSDLLL VQSDL YTLVDGFVTR VPLVLMNSFNT HDDTQKIVEK + Oxidation (M) SAVDGLTEMSENEKSGFINLVR	46%
442 12S seed storage protein [Precursor]	At5g44120	CSGVSFAR + Carbamidomethyl (C) CTDNLDDPSR + Carbamidomethyl (C) GLYLPSSFFNTAK VIPGCAETFQDSSEFQPR + Carbamidomethyl (C) GLPLEVITNGFQISPEEAR IDLQTAQQQLQNQDDNRGNIVR VQGPFGVIRPPLRGQRPQE EEEEEEGR	24%
498 Beta-cruciferin 12S (seed storage protein At4g28520 fragment)		ADVYKPSLGR FNTLETTLTR GVLQGNAMVLPK TNENAMISTLAGR IKFNTLETTLTR VTSVNSYTLPILEYVR YNMMANEILYCTGGQGR IQVVNDNGQNVLDDQQVQK ALPLEVISNGFQISPEEAR SHENIDDPARADVYKPSLGR	79%
